

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/647,965

DATE: 07/05/2001

TIME: 16:22:13

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF3\07032001\I647965.raw

C--> 3 <110> APPLICANT: Hiscott, John  
 4 Lin, Rongtuan  
 6 <120> TITLE OF INVENTION: HIGHLY ACTIVE FORMS OF INTERFERON  
 7 REGULATORY FACTOR PROTEINS  
 9 <130> FILE REFERENCE: A33606-PCT-USA 071235.0111  
 11 <140> CURRENT APPLICATION NUMBER: US 09/647,965  
 12 <141> CURRENT FILING DATE: 2001-05-24  
 14 <150> PRIOR APPLICATION NUMBER: PCT/CA99/00314  
 15 <151> PRIOR FILING DATE: 1999-04-07  
 17 <150> PRIOR APPLICATION NUMBER: CA 2,234,588  
 18 <151> PRIOR FILING DATE: 1998-04-07  
 20 <160> NUMBER OF SEQ ID NOS: 11  
 22 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 1284  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: Homo sapiens  
 29 <220> FEATURE:  
 30 <221> NAME/KEY: CDS  
 31 <222> LOCATION: (1)...(1284)  
 33 <400> SEQUENCE: 1  
 34 atg gga acc cca aag cca cgg atc ctg ccc tgg ctg gtg tcg cag ctg 48  
 35 Met Gly Thr Pro Lys Pro Arg Ile Leu Pro Trp Leu Val Ser Gln Leu  
 36 1 5 10 15  
 38 gac ctg ggg caa ctg gag ggc gtg gcc tgg gtg aac aag agc cgc acg 96  
 39 Asp Leu Gly Gln Leu Glu Gly Val Ala Trp Val Asn Lys Ser Arg Thr  
 40 20 25 30  
 42 cgc ttc cgc atc cct tgg aag cac ggc cta cgg cag gat gca cag cag 144  
 43 Arg Phe Arg Ile Pro Trp Lys His Gly Leu Arg Gln Asp Ala Gln Gln  
 44 35 40 45  
 46 gag gat ttc gga atc ttc cag gcc tgg gcc gag gcc act ggt gca tat 192  
 47 Glu Asp Phe Gly Ile Phe Gln Ala Trp Ala Glu Ala Thr Gly Ala Tyr  
 48 50 55 60  
 50 gtt ccc ggg agg gat aag cca gac ctg cca acc tgg aag agg aat ttc 240  
 51 Val Pro Gly Arg Asp Lys Pro Asp Leu Pro Thr Trp Lys Arg Asn Phe  
 52 65 70 75 80  
 54 cgc tct gcc ctc aac cgc aaa gaa ggg ttg cgt tta gca gag gac cgg 288  
 55 Arg Ser Ala Leu Asn Arg Lys Glu Gly Leu Arg Leu Ala Glu Asp Arg  
 56 85 90 95  
 58 agc aag gac cct cac gac cca cat aaa atc tac gag ttt gtg aac tca 336  
 59 Ser Lys Asp Pro His Asp Pro His Lys Ile Tyr Glu Phe Val Asn Ser  
 60 100 105 110  
 62 gga gtt ggg gac ttt tcc cag cca gac acc tct ccg gac acc aat ggt 384  
 63 Gly Val Gly Asp Phe Ser Gln Pro Asp Thr Ser Pro Asp Thr Asn Gly  
 64 115 120 125  
 66 gga ggc agt act tct gat acc cag gaa gac att ctg gat gag tta ctg 432  
 67 Gly Gly Ser Thr Ser Asp Thr Gln Glu Asp Ile Leu Asp Glu Leu Leu

ENTERED

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68	130	135	140	
70	ggt aac atg gtg ttg gcc cca ctc cca gat ccg gga ccc cca agc ctg	480		
71	Gly Asn Met Val Leu Ala Pro Leu Pro Asp Pro Gly Pro Pro Ser Leu			
72	145 150 155 160			
74	gct gta gcc cct gag ccc tgc cct cag ccc ctg cgg agc ccc agc ttg	528		
75	Ala Val Ala Pro Glu Pro Cys Pro Gln Pro Leu Arg Ser Pro Ser Leu			
76	165 170 175			
78	gac aat ccc act ccc ttc cca aac ctg ggg ccc tct gag aac cca ctg	576		
79	Asp Asn Pro Thr Pro Phe Pro Asn Leu Gly Pro Ser Glu Asn Pro Leu			
80	180 185 190			
82	aag cgg ctg ttg gtg ccg ggg gaa gag tgg gag ttc gag gtg aca gcc	624		
83	Lys Arg Leu Leu Val Pro Gly Glu Glu Trp Glu Phe Glu Val Thr Ala			
84	195 200 205			
86	ttc tac cgg ggc cgc caa gtc ttc cag cag acc atc tcc tgc ccg gag	672		
87	Phe Tyr Arg Gly Arg Gln Val Phe Gln Gln Thr Ile Ser Cys Pro Glu			
88	210 215 220			
90	ggc ctg cgg ctg gtg ggg tcc gaa gtg gga gac agg acg ctg cct gga	720		
91	Gly Leu Arg Leu Val Gly Ser Glu Val Gly Asp Arg Thr Leu Pro Gly			
92	225 230 235 240			
94	tgg cca gtc aca ctg cca gac cct ggc atg tcc ctg aca gac agg gga	768		
95	Trp Pro Val Thr Leu Pro Asp Pro Gly Met Ser Leu Thr Asp Arg Gly			
96	245 250 255			
98	gtg atg agc tac gtg agg cat gtg ctg agc tgc ctg ggt ggg gga ctg	816		
99	Val Met Ser Tyr Val Arg His Val Leu Ser Cys Leu Gly Gly Gly Leu			
100	260 265 270			
102	gct ctc tgg cgg gcc ggg cag tgg ctc tgg gcc cag cgg ctg ggg cac	864		
103	Ala Leu Trp Arg Ala Gly Gln Trp Leu Trp Ala Gln Arg Leu Gly His			
104	275 280 285			
106	tgc cac aca tac tgg gca gtg agc gag gag ctg ctc ccc aac agc ggg	912		
107	Cys His Thr Tyr Trp Ala Val Ser Glu Glu Leu Leu Pro Asn Ser Gly			
108	290 295 300			
110	cat ggg cct gat ggc gag gtc ccc aag gac aag gaa gga ggc gtg ttt	960		
111	His Gly Pro Asp Gly Glu Val Pro Lys Asp Lys Glu Gly Gly Val Phe			
112	305 310 315 320			
114	gac ctg ggg ccc ttc att gta gat ctg att acc ttc acg gaa gga agc	1008		
115	Asp Leu Gly Pro Phe Ile Val Asp Leu Ile Thr Phe Thr Glu Gly Ser			
116	325 330 335			
118	gga cgc tca cca cgc tat gcc ctc tgg ttc tgt gtg ggg gag tca tgg	1056		
119	Gly Arg Ser Pro Arg Tyr Ala Leu Trp Phe Cys Val Gly Glu Ser Trp			
120	340 345 350			
122	ccc cag gac cag ccg tgg acc aag agg ctc gtg atg gtc aag gtt gtg	1104		
123	Pro Gln Asp Gln Pro Trp Thr Lys Arg Leu Val Met Val Lys Val Val			
124	355 360 365			
126	ccc acg tgc ctc agg gcc ttg gta gaa atg gcc cgg gta ggg ggt gcc	1152		
127	Pro Thr Cys Leu Arg Ala Leu Val Glu Met Ala Arg Val Gly Gly Ala			
128	370 375 380			
130	tcc tcc ctg gag aat act gtg gac ctg cac att gac aac gac cac cca	1200		
131	Ser Ser Leu Glu Asn Thr Val Asp Leu His Ile Asp Asn Asp His Pro			
132	385 390 395 400			

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```

134 ctc gac ctc gac gac gac cag tac aag gcc tac ctg cag gac ttg gtg      1248
135 Leu Asp Leu Asp Asp Asp Gln Tyr Lys Ala Tyr Leu Gln Asp Leu Val
136                               405                               410           415
138 gag ggc atg gat ttc cag ggc cct ggg gag agc tga                        1284
139 Glu Gly Met Asp Phe Gln Gly Pro Gly Glu Ser *
140                               420                               425
143 <210> SEQ ID NO: 2
144 <211> LENGTH: 427
145 <212> TYPE: PRT
146 <213> ORGANISM: Homo sapiens
148 <400> SEQUENCE: 2
149 Met Gly Thr Pro Lys Pro Arg Ile Leu Pro Trp Leu Val Ser Gln Leu
150 1 5 10 15
151 Asp Leu Gly Gln Leu Glu Gly Val Ala Trp Val Asn Lys Ser Arg Thr
152 20 25 30
153 Arg Phe Arg Ile Pro Trp Lys His Gly Leu Arg Gln Asp Ala Gln Gln
154 35 40 45
155 Glu Asp Phe Gly Ile Phe Gln Ala Trp Ala Glu Ala Thr Gly Ala Tyr
156 50 55 60
157 Val Pro Gly Arg Asp Lys Pro Asp Leu Pro Thr Trp Lys Arg Asn Phe
158 65 70 75 80
159 Arg Ser Ala Leu Asn Arg Lys Glu Gly Leu Arg Leu Ala Glu Asp Arg
160 85 90 95
161 Ser Lys Asp Pro His Asp Pro His Lys Ile Tyr Glu Phe Val Asn Ser
162 100 105 110
163 Gly Val Gly Asp Phe Ser Gln Pro Asp Thr Ser Pro Asp Thr Asn Gly
164 115 120 125
165 Gly Gly Ser Thr Ser Asp Thr Gln Glu Asp Ile Leu Asp Glu Leu Leu
166 130 135 140
167 Gly Asn Met Val Leu Ala Pro Leu Pro Asp Pro Gly Pro Pro Ser Leu
168 145 150 155 160
169 Ala Val Ala Pro Glu Pro Cys Pro Gln Pro Leu Arg Ser Pro Ser Leu
170 165 170 175
171 Asp Asn Pro Thr Pro Phe Pro Asn Leu Gly Pro Ser Glu Asn Pro Leu
172 180 185 190
173 Lys Arg Leu Leu Val Pro Gly Glu Glu Trp Glu Phe Glu Val Thr Ala
174 195 200 205
175 Phe Tyr Arg Gly Arg Gln Val Phe Gln Gln Thr Ile Ser Cys Pro Glu
176 210 215 220
177 Gly Leu Arg Leu Val Gly Ser Glu Val Gly Asp Arg Thr Leu Pro Gly
178 225 230 235 240
179 Trp Pro Val Thr Leu Pro Asp Pro Gly Met Ser Leu Thr Asp Arg Gly
180 245 250 255
181 Val Met Ser Tyr Val Arg His Val Leu Ser Cys Leu Gly Gly Gly Leu
182 260 265 270
183 Ala Leu Trp Arg Ala Gly Gln Trp Leu Trp Ala Gln Arg Leu Gly His
184 275 280 285
185 Cys His Thr Tyr Trp Ala Val Ser Glu Glu Leu Leu Pro Asn Ser Gly
186 290 295 300

```

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```

187 His Gly Pro Asp Gly Glu Val Pro Lys Asp Lys Glu Gly Gly Val Phe
188 305                      310                      315                      320
189 Asp Leu Gly Pro Phe Ile Val Asp Leu Ile Thr Phe Thr Glu Gly Ser
190                      325                      330                      335
191 Gly Arg Ser Pro Arg Tyr Ala Leu Trp Phe Cys Val Gly Glu Ser Trp
192                      340                      345                      350
193 Pro Gln Asp Gln Pro Trp Thr Lys Arg Leu Val Met Val Lys Val Val
194                      355                      360                      365
195 Pro Thr Cys Leu Arg Ala Leu Val Glu Met Ala Arg Val Gly Gly Ala
196                      370                      375                      380
197 Ser Ser Leu Glu Asn Thr Val Asp Leu His Ile Asp Asn Asp His Pro
198 385                      390                      395                      400
199 Leu Asp Leu Asp Asp Asp Gln Tyr Lys Ala Tyr Leu Gln Asp Leu Val
200                      405                      410                      415
201 Glu Gly Met Asp Phe Gln Gly Pro Gly Glu Ser
202                      420                      425

```

205 &lt;210&gt; SEQ ID NO: 3

206 &lt;211&gt; LENGTH: 13

207 &lt;212&gt; TYPE: PRT

208 &lt;213&gt; ORGANISM: Homo sapiens

210 &lt;400&gt; SEQUENCE: 3

211 Ile Ser Asn Ser His Pro Leu Ser Leu Thr Ser Asp Gln

212 1 5 10

215 &lt;210&gt; SEQ ID NO: 4

216 &lt;211&gt; LENGTH: 4

217 &lt;212&gt; TYPE: PRT

218 &lt;213&gt; ORGANISM: Homo sapiens

220 &lt;400&gt; SEQUENCE: 4

221 Gly Ala Ala Ala

222 1

225 &lt;210&gt; SEQ ID NO: 5

226 &lt;211&gt; LENGTH: 6

227 &lt;212&gt; TYPE: PRT

228 &lt;213&gt; ORGANISM: Homo sapiens

230 &lt;400&gt; SEQUENCE: 5

231 Gly Ala Ala Ala Asn Asn

232 1 5

235 &lt;210&gt; SEQ ID NO: 6

236 &lt;211&gt; LENGTH: 15

237 &lt;212&gt; TYPE: DNA

238 &lt;213&gt; ORGANISM: Homo sapiens

240 &lt;400&gt; SEQUENCE: 6

241 ggaaaactga aaggg

15

243 &lt;210&gt; SEQ ID NO: 7

244 &lt;211&gt; LENGTH: 30

245 &lt;212&gt; TYPE: DNA

246 &lt;213&gt; ORGANISM: Homo sapiens

248 &lt;400&gt; SEQUENCE: 7

249 gatcgggaaa gggaaaccga aactgaagcc

30

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251 <210> SEQ ID NO: 8
252 <211> LENGTH: 1512
253 <212> TYPE: DNA
254 <213> ORGANISM: Homo sapiens
256 <220> FEATURE:
257 <221> NAME/KEY: CDS
258 <222> LOCATION: (1)...(1512)
260 <400> SEQUENCE: 8
261 atg gcc ttg gct cct gag agg gca gcc cca cgc gtg ctg ttc gga gag 48
262 Met Ala Leu Ala Pro Glu Arg Ala Ala Pro Arg Val Leu Phe Gly Glu
263 1 5 10 15
265 tgg ctc ctt gga gag atc agc agc ggc tgc tat gag ggg ctg cag tgg 96
266 Trp Leu Leu Gly Glu Ile Ser Ser Gly Cys Tyr Glu Gly Leu Gln Trp
267 20 25 30
269 ctg gac gag gcc cgc acc tgt ttc cgc gtg ccc tgg aag cac ttc gcg 144
270 Leu Asp Glu Ala Arg Thr Cys Phe Arg Val Pro Trp Lys His Phe Ala
271 35 40 45
273 cgc aag gac ctg agc gag gcc gac gcg cgc atc ttc aag gcc tgg gct 192
274 Arg Lys Asp Leu Ser Glu Ala Asp Ala Arg Ile Phe Lys Ala Trp Ala
275 50 55 60
277 gtg gcc cgc ggc agg tgg ccg cct agc agc agg gga ggt ggc ccg ccc 240
278 Val Ala Arg Gly Arg Trp Pro Pro Ser Ser Arg Gly Gly Gly Pro Pro
279 65 70 75 80
281 ccc gag gct gag act gcg gag cgc gcc ggc tgg aaa acc aac ttc cgc 288
282 Pro Glu Ala Glu Thr Ala Glu Arg Ala Gly Trp Lys Thr Asn Phe Arg
283 85 90 95
285 tgc gca ctg cgc agc acg cgt cgc ttc gtg atg ctg cgg gat aac tcg 336
286 Cys Ala Leu Arg Ser Thr Arg Arg Phe Val Met Leu Arg Asp Asn Ser
287 100 105 110
289 ggg gac ccg gcc gac ccg cac aag gtg tac gcg ctc agc cgg gag ctg 384
290 Gly Asp Pro Ala Asp Pro His Lys Val Tyr Ala Leu Ser Arg Glu Leu
291 115 120 125
293 tgc tgg cga gaa ggc cca ggc acg gac cag act gag gca gag gcc ccc 432
294 Cys Trp Arg Glu Gly Pro Gly Thr Asp Gln Thr Glu Ala Glu Ala Pro
295 130 135 140
297 gca gct gtc cca cca cca cag ggt ggg ccc cca ggg cca ttc ttg gca 480
298 Ala Ala Val Pro Pro Pro Gln Gly Gly Pro Pro Gly Pro Phe Leu Ala
299 145 150 155 160
301 cac aca cat gct gga ctc caa gcc cca ggc ccc ctc cct gcc cca gct 528
302 His Thr His Ala Gly Leu Gln Ala Pro Gly Pro Leu Pro Ala Pro Ala
303 165 170 175
305 ggt gac aag ggg gac ctc ctg ctc cag gca gtg caa cag agc tgc ctg 576
306 Gly Asp Lys Gly Asp Leu Leu Leu Gln Ala Val Gln Gln Ser Cys Leu
307 180 185 190
309 gca gac cat ctg ctg aca gcg tca tgg ggg gca gat cca gtc cca acc 624
310 Ala Asp His Leu Leu Thr Ala Ser Trp Gly Ala Asp Pro Val Pro Thr
311 195 200 205
313 aag gct cct gga gag gga caa gaa ggg ctt ccc ctg act ggg gcc tgt 672
314 Lys Ala Pro Gly Glu Gly Gln Glu Gly Leu Pro Leu Thr Gly Ala Cys

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/647,965

DATE: 07/05/2001

TIME: 16:22:14

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF3\07032001\I647965.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date